

# Sequence Listing

<110> ASHKENAZI, AVI J  
 BOTSTEIN, DAVID  
 DODGE, KELLY H.  
 GURNEY, AUSTIN L.  
 KIM, KYUNG JIN  
 LAWRENCE, DAVID A.  
 PITTI, ROBERT  
 ROY, MARGARET A  
 TUMAS, DANIEL B  
 WOOD, WILLIAM I.

<120> Dcr3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289

<141> 1998-09-18

<150> US 60/059,288

<151> 1997-09-18

<150> US 60/094,640

<151> 1998-07-30

<160> 18

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<212> PRT

<213> Homo sapiens

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			20					25					30	

Ala	Glu	Thr	Pro	Thr	Tyr	Pro	Trp	Arg	Asp	Ala	Glu	Thr	Gly	Glu
			35					40					45	

Arg	Leu	Val	Cys	Ala	Gln	Cys	Pro	Pro	Gly	Thr	Phe	Val	Gln	Arg
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Pro	Cys	Arg	Arg	Asp	Ser	Pro	Thr	Thr	Cys	Gly	Pro	Cys	Pro	Pro
			65					70					75	

Arg	His	Tyr	Thr	Gln	Phe	Trp	Asn	Tyr	Leu	Glu	Arg	Cys	Arg	Tyr
			80					85					90	

Cys	Asn	Val	Leu	Cys	Gly	Glu	Arg	Glu	Glu	Glu	Ala	Arg	Ala	Cys	95	100	105
His	Ala	Thr	His	Asn	Arg	Ala	Cys	Arg	Cys	Arg	Thr	Gly	Phe	Phe	110	115	120
Ala	His	Ala	Gly	Phe	Cys	Leu	Glu	His	Ala	Ser	Cys	Pro	Pro	Gly	125	130	135
Ala	Gly	Val	Ile	Ala	Pro	Gly	Thr	Pro	Ser	Gln	Asn	Thr	Gln	Cys	140	145	150
Gln	Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Ala	Ser	Ser	Ser	Ser	Ser	155	160	165
Glu	Gln	Cys	Gln	Pro	His	Arg	Asn	Cys	Thr	Ala	Leu	Gly	Leu	Ala	170	175	180
Leu	Asn	Val	Pro	Gly	Ser	Ser	Ser	His	Asp	Thr	Leu	Cys	Thr	Ser	185	190	195
Cys	Thr	Gly	Phe	Pro	Leu	Ser	Thr	Arg	Val	Pro	Gly	Ala	Glu	Glu	200	205	210
Cys	Glu	Arg	Ala	Val	Ile	Asp	Phe	Val	Ala	Phe	Gln	Asp	Ile	Ser	215	220	225
Ile	Lys	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu	Ala	Pro	Glu	230	235	240
Gly	Trp	Gly	Pro	Thr	Pro	Arg	Ala	Gly	Arg	Ala	Ala	Leu	Gln	Leu	245	250	255
Lys	Leu	Arg	Arg	Arg	Leu	Thr	Glu	Leu	Leu	Gly	Ala	Gln	Asp	Gly	260	265	270
Ala	Leu	Leu	Val	Arg	Leu	Leu	Gln	Ala	Leu	Arg	Val	Ala	Arg	Met	275	280	285
Pro	Gly	Leu	Glu	Arg	Ser	Val	Arg	Glu	Arg	Phe	Leu	Pro	Val	His	290	295	300

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atgagggcgc tggagggggc aggctgtcg ctgctgtgcc tgggtgttggc 150  
gctgcctgcc ctgctgccgg tgccggctgt acgcggagtg gcagaaacac 200  
ccacctaccc ctggcgggac gcagagacag gggagcggct ggtgtgcgcc 250  
cagtgcctcc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300  
cacgacgtgt ggcccgtgtc caccgcgcca ctacacgcag ttctggaact 350  
acctggagcg ctgccgctac tgcaacgtcc tctgcgggga gcgtgaggag 400  
gaggcacggg cttgccacgc caccacaaac cgtgcctgcc gctgccgcac 450  
cggcttcttc ggcacgctg gtttctgctt ggagcacgca tcgtgtccac 500  
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cagccgtgcc ccccaggcac cttctcagcc agcagctcca gctcagagca 600  
gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc 650  
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ctcagcacca ggggtaccagg agctgaggag tgtgagcgtg ccgtcatcga 750  
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aggccctcga ggccccggag ggctggggtc cgacaccaag ggcgggccgc 850  
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tgatcctggc cccctcttat ttattctaca tccttggcac ccacttgca 1050  
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ggagcgtgag gaggaggcac gggcttgcca cgccaccac aaccgtgcct 150  
  
gccgctgccg caccggttc ttcgcgcacg ctggtttctg cttggagcac 200  
  
gcatcgtgtc cacctggtgc cggcgtgatt gcccgggca cccccagcca 250  
  
gaacacgcag tgcctagccg tgccccccag gcaccttctc agccagcagc 300  
  
tccagctcag agcagtgcc accccaccgc aactgcacgg ccctgggcct 350  
  
ggccctcaat gtgccaggt cttcctcca tgacaccctg tgcaccagct 400  
  
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ggagcntgag gaggaggcan gngcttgcca cgccacccac aaccgcgcct 150

gngctgcag caccgnttc ttgcgcacg ctgntttctg cttggagcac 200

gcacgtgtc cacctggtgn cggcgtgatt gncccgggca cccccagcca 250

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<213> Unknown

<223> Unknown organism

<221> unsure

<222> 182

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tgccgctgcc gcaccggctt cttegcgcac gctggtttct gcttggagca 150

cgcacgtgtg ccacctgggtg ccggcgtgat tnccecgggc acccccagcc 200

a 201

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cttcctcct ggtgcaggc accccagcc agaacacgca gnccagccgt 150  
gccccccagg caccttctca gccagcagct ccagctcaga gcagtgccag 200  
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ccagctcaga gcagtgccag cccccaccgca actgcacggc cctgggcctg 150  
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ccc 53

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<212> PRT  
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35 40 45  
Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly  
50 55 60  
Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys  
65 70 75  
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val  
80 85 90  
Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val  
95 100 105  
Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys  
110 115 120  
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg  
125 130 135  
Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala  
140 145 150  
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala  
155 160 165  
Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg  
170 175 180  
Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser  
185 190 195  
Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala  
200 205 210

Pro Gly Ala Val	His Leu Pro Gln Pro	Val Ser Thr Arg Ser Gln
215	220	225
His Thr Gln Pro	Thr Pro Glu Pro Ser	Thr Ala Pro Ser Thr Ser
230	235	240
Phe Leu Leu Pro	Met Gly Pro Ser Pro	Pro Ala Glu Gly Ser Thr
245	250	255
Gly Asp Phe Ala	Leu Pro Val Gly Leu	Ile Val Gly Val Thr Ala
260	265	270
Leu Gly Leu Leu	Ile Ile Gly Val Val	Asn Cys Val Ile Met Thr
275	280	285
Gln Val Lys Lys	Lys Pro Leu Cys Leu	Gln Arg Glu Ala Lys Val
290	295	300
Pro His Leu Pro	Ala Asp Lys Ala Arg	Gly Thr Gln Gly Pro Glu
305	310	315
Gln Gln His Leu	Leu Ile Thr Ala Pro	Ser Ser Ser Ser Ser Ser
320	325	330
Leu Glu Ser Ser	Ala Ser Ala Leu Asp	Arg Arg Ala Pro Thr Arg
335	340	345
Asn Gln Pro Gln	Ala Pro Gly Val Glu	Ala Ser Gly Ala Gly Glu
350	355	360
Ala Arg Ala Ser	Thr Gly Ser Ser Asp	Ser Ser Pro Gly Gly His
365	370	375
Gly Thr Gln Val	Asn Val Thr Cys Ile	Val Asn Val Cys Ser Ser
380	385	390
Ser Asp His Ser	Ser Gln Cys Ser Ser	Gln Ala Ser Ser Thr Met
395	400	405
Gly Asp Thr Asp	Ser Ser Pro Ser Glu	Ser Pro Lys Asp Glu Gln
410	415	420
Val Pro Phe Ser	Lys Glu Glu Cys Ala	Phe Arg Ser Gln Leu Glu
425	430	435
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455	460	

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				20					25					30	
Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	
				35					40					45	
Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	
				50					55					60	
Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	
				65					70					75	
Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	
				80					85					90	
Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	
				95					100					105	
Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	
				110					115					120	
His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	
				125					130					135	
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	
				140					145					150	
Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	
				155					160					165	
Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	
				170					175					180	
His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	
				185					190					195	
Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	
				200					205					210	
Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	
				215					220					225	

05996096-063801

Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys  
245 250 255

Leu Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile  
260 265 270

Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile  
275 280 285

Gly His Ala Asn Leu Thr Phe Glu  
290

0906096-062801